

Supplementary file 1

List of hepatitis E virus sequences analysed with genotype and subtype designation.

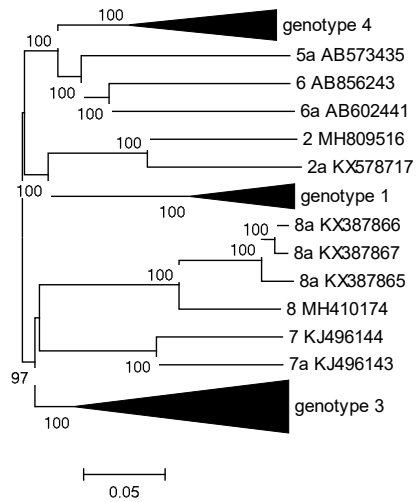
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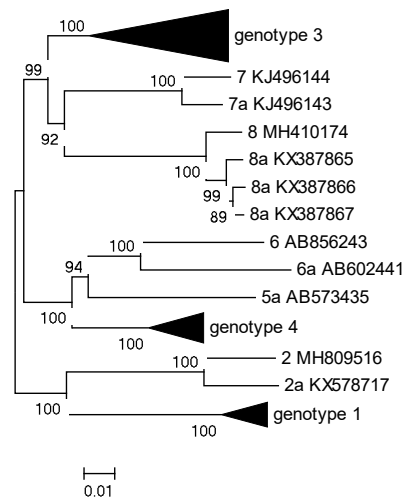
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Supplementary Figure 1

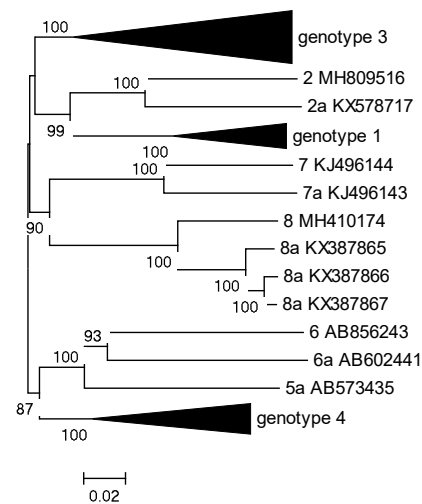
(a) ORF1 nt



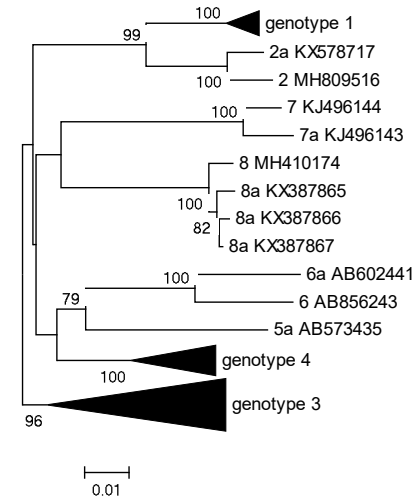
(b) ORF1 aa



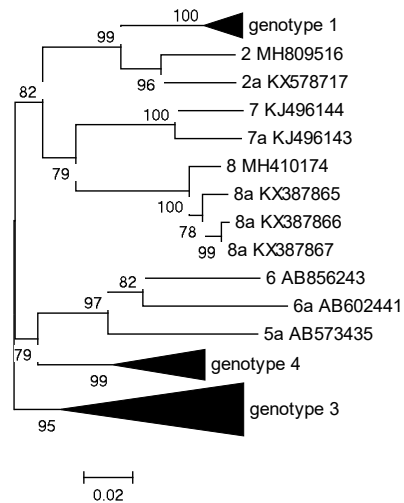
(c) ORF2 nt



(d) ORF2 aa



(e) ORF3 nt



(f) ORF3 aa

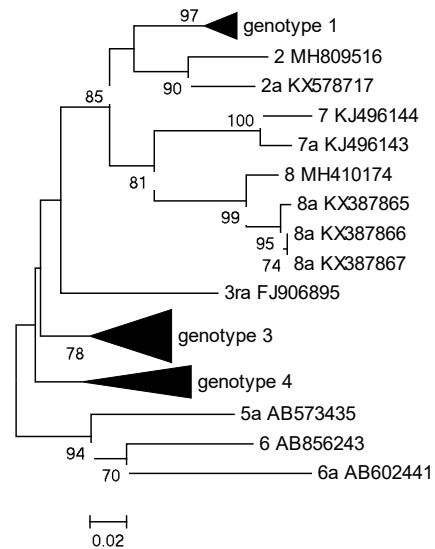


Figure legend Supplementary Figure 1

Phylogenetic analysis of hepatitis E virus ORFs 1–3. Aligned nucleotide (a, c, e) or amino acid (b, d, f) sequences of ORF1 (a, b), ORF2 (c, d) or ORF3 (e, f) of HEV reference strains as detailed in Table 1 were used to produced neighbour-joining phylogenetic trees using MEGA7 (Kumar *et al.*, 2016). Trees were based on Jukes-Cantor distances (nucleotide sequences) or p-distances (amino acid sequences). The branches for genotypes 1, 3 and 4 have been collapsed. Numbers indicate bootstrap support where this was >70% (1000 replicates).